

OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:23:49 ; Search time 3936 Seconds  
(Without alignments)  
10417.304 Million cell updates/sec

Title: US-09-922-378-1  
Perfect score: 946  
Sequence: 1 gggcctaggcgccgggtca.....gtgtgcacaaaaa 946

Scoring table: IDENTITY.NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_bai.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
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- 27: em\_sts.\*

- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_lrv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rtd.\*
- 36: em\_htg\_nam.\*
- 37: em\_htg\_vit.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	946	100.0	946	6 AR274069	AR274069 Sequence
3	946	100.0	946	6 AX164659	AX164659 Sequence
4	946	100.0	946	6 BD062636	BD062636 Homo sapi
5	845	89.3	935	9 BC001901	BC001901 Homo sapi
6	840.4	88.8	1105	6 AR100664	AR100664 Sequence
7	840.4	88.8	1105	6 AR166571	AR166571 Sequence
8	835.4	88.3	899	9 AF021792	AF021792 Homo sapi
9	799	84.5	953	6 AX329750	AX329750 Sequence
10	799	84.5	953	9 HSU66879	U66879 Human Bcl-2
11	799	84.5	971	6 AR380101	AR380101 Sequence
12	737	77.9	944	6 I63695	I63695 Sequence 1
13	507	53.6	507	6 AX057144	AX057144 Sequence
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37 226.8 24.0 779 10 AF279911  
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40 197 20.8 230039 2 AC090391  
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ALIGNMENTS

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LOCUS AR079500 946 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 1 from patent US 5965703.  
ACCESSION AR079500  
VERSION AR079500.1 GI:10006244  
KEYWORDS  
SOURCE  
ORGANISM

Unclassified.  
REFERENCE 1 (bases 1 to 946)  
AUTHORS Horne,W.A. and Oltersdorf,T.  
TITLE Human bad polypeptides, encoding nucleic acids and methods of use  
JOURNAL Patent: US 5965703-A 1 12-OCT-1999;  
FEATURES  
Location/Qualifiers  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.5e-186;  
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGCTAGGGCCCGGCTCAGGGGCTTGGGCGCCAGAGCATGTTCCAG 60  
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LOCUS AR274069 946 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 650402.  
ACCESSION AR274069  
VERSION AR274069.1 GI:29706040  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 946)  
AUTHORS Horne, W.A. and Oltersdorf, T.  
TITLE Human bad polypeptides, encoding nucleic acids and methods of use  
JOURNAL Patent: US 6504022-A 1 07-JAN-2003;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 946; DB 6; Length 946;  
Best Local Similarity 100.0%; Pred. No. 4.5e-186;  
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 3  
AX164659 946 bp DNA linear PAT 22-JUN-2001  
LOCUS Sequence 1 from Patent EP1097994.  
ACCESSION AX164659  
VERSION AX164659.1 GI:14545564  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Oltersdorf, T.  
TITLE Human bad polypeptides, encoding nucleic acids and methods of use  
JOURNAL Patent: EP 1097994-A 1 09-MAY-2001;  
Idun Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 946; DB 6; Length 946;  
Best Local Similarity 100.0%; Pred. No. 4.5e-186;  
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
BD062656  
LOCUS Human BAD polypeptides, encoding nucleic acids and methods of use.  
DEFINITION Human BAD polypeptides, encoding nucleic acids and methods of use.  
ACCESSION BD062656  
VERSION BD062656.1 GI:22608259  
KEYWORDS JP 2001507211-A/1.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 946)  
AUTHORS Horne, W.A. and Oltersdorf, T.  
TITLE Human BAD polypeptides, encoding nucleic acids and methods of use  
JOURNAL Patent: JP 2001507211-A 1 05-JUN-2001;  
IDUN PHARMACEUTICALS INC  
COMMENT PN JP 2001507211-A/1  
PD 05-JUN-2001  
PF 18-SEP-1997 JP 1998514997  
PR 20-SEP-1996 US 08/717123  
PI WILLIAM A HORNE, TILMAN OLTERSDORF  
PC CL2N15/09, A61K45/00, A61P43/00, C07K14/47, C12Q1/02, G01N33/15, PC  
G01N33/50.

PC CL2N15/00  
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Best Local Similarity 100.0%; Pred. No. 4.5e-186;  
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCTAGGGGCGCGGCTCAGGGGCTTCAGAGATCGGGCTTTGGGCCCCCAGAGCATGTTCAG 60  
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Qy	901	GTACCAATGTTAATAAGCCCGCTGTGTGCCAAAAA 946	

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:19:03 ; Search time 460 Seconds  
(without alignments)  
8736.512 Million cell updates/sec

Title: US-09-922-378-1  
Perfect score: 946  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues 6747726

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
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10: Geneseqn2004s:\*

AB281200

AB281200 standard; cDNA; 945 BP.

XX AB281200;

AC

XX

DT 10-MAY-2003 (first entry)

XX

DE Human BAD encoding cDNA SEQ ID NO:1.

XX

KW Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;

XX

XX virucide; infection; gene; ss.

XX

OS Homo sapiens.

ALIGNMENTS

RESULT 1

Result No.	Score	Query Match Length	ID	Description
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4	840.4	88.8	1105 4 AAH78430	AAH78430 Nucleotid
5	799	84.5	953 6 ABL61922	ABL61922 Colon ade
6	737	77.9	944 2 AAT91561	AAT91561 BGC5 Gene
7	546	57.7	842 6 ABQ54707	ABQ54707 Human ova

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AB281200

AB281200 standard; cDNA; 945 BP.

XX AB281200;

AC

XX

DT 10-MAY-2003 (first entry)

XX

DE Human BAD encoding cDNA SEQ ID NO:1.

XX

KW Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;

XX

XX virucide; infection; gene; ss.

XX

OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 52..558  
FT /\*tag= a  
FT /product= "BAD protein"

XX PN WO2003012049-A2.

XX PD 13-FEB-2003.

XX PF 31-JUL-2002; 2002WO-US024177.

XX PR 31-JUL-2001; 2001US-0308929P.

XX PA (UYCH-) UNIV CHICAGO.

XX PI Munger J, Roizman B;

XX DR WPI; 2003-248168/24.

XX DR P-PSDB; ABR39081.

XX PT Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by  
PT administering to the cell, a composition comprising an agent that  
PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3.

XX PS Disclosure; Page 165-166; 192pp; English.

XX CC The present invention describes a method (M1) for inducing apoptosis in a  
CC cell infected with herpes simplex virus (HSV), which comprises  
CC administering to the cell, a composition having an agent that inhibits  
CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also  
CC described is a method (M2) for treating a patient infected with HSV, by  
CC administering to the patient, a composition comprising a peptide  
CC comprising a sequence of 4-100 continuous amino acids of a 168 residue  
CC amino acid sequence (see ABR39081), where the peptide comprises ser112,  
CC ser135, or ser155, or their combinations. BAD has virucide activity. M1  
CC is useful for inducing apoptosis in a cell infected with HSV, where the  
CC cell is in a human. M2 is useful for treating a patient infected with  
CC HSV. The present sequence encodes human BAD, which is given in the  
CC exemplification of the present invention

XX SQ Sequence 945 BP; 185 A; 294 C; 309 G; 157 T; 0 U; 0 Other;

Query Match 99.98; Score 945; DB 7; Length 945;

Best Local Similarity 100.0%; Pred. No. 1.4e-225;

Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTAGGGCGCGGCTCAGGGGCTCGAGATCGGGCTTGGGCCAGAGCATGTTCCAG 60

DB 1 GGGCTAGGGCGCGGCTCAGGGGCTCGAGATCGGGCTTGGGCCAGAGCATGTTCCAG 60

QY 61 ATCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTTCGACAGAGGGGCTTGGGC 120

DB 61 ATCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTTCGACAGAGGGGCTTGGGC 120

QY 121 CCCAGCCCGCAGGGGACGGGCTTCAGGCTCCGGCAGCATCATCGCCGCCCCCAGGC 180

DB 121 CCCAGCCCGCAGGGGACGGGCTTCAGGCTTCGGCAAGCATCATCGCCAGGCCCCAGGC 180

QY 181 CTCCTGTGGGACGGCCAGTCCACAGCAGGAGCAGCCCAACCCAGCAGCAGCATCATGGAGCC 240

DB 181 CTCCTGTGGGACGGCCAGTCCACAGCAGGAGCAGCCCAACCCAGCAGCAGCATCATGGAGCC 240

QY 241 GCTGGGCTCTGTGAGATCCGGAGTCCGCCACAGCTTCCTACCCCGCGGGGAGCAGGACAC 300

DB 241 GCTGGGCTCTGTGAGATCCGGAGTCCGCCACAGCTTCCTACCCCGCGGGGAGCAGGACAC 300

QY 301 GAAGGATGGGGAGGAGCCAGCCCTTTGGGGGCGGCTCGGCTCGGGGCCCCCCCCAAC 360

DB 301 GAAGGATGGGGAGGAGCCAGCCCTTTGGGGGCGGCTCGGCTCGGGGCCCCCCCCAAC 360

QY 361 CTCGGGACGACACAGCGCTATGCGCGGAGCTCCGGAGGATGAGTGACGAGTTTGTGGAC 420

DB 361 CTCGGGACGACACAGCGCTATGCGCGGAGCTCCGGAGGATGAGTGACGAGTTTGTGGAC 420

QY 421 TCTTTAAGAGGAGACTTCTCCGCCGAGAGCGCGGGCAGACGACAGCAGATCGGCAA 480

DB 421 TCTTTAAGAGGAGACTTCTCCGCCGAGAGCGCGGGCAGACGACAGCAGATCGGCAA 480

QY 481 AGCTCCAGCTGGACGGAGTCTTCCAGTCTCTGAGTGGGATCGGAATCTGGCAGGGAGGC 540

DB 481 AGCTCCAGCTGGACGGAGTCTTCCAGTCTCTGAGTGGGATCGGAATCTGGCAGGGAGGC 540

QY 541 TCCGCCCTCTCCAGTGACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTTGCCCT 600

DB 541 TCCGCCCTCTCCAGTGACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTTGCCCT 600

QY 601 GGGAGCATTTTGAATATGGGAGGAGTAAAGTTCCCTCAGGCTATGCAAAAAGAGAT 660

DB 601 GGGAGCATTTTGAATATGGGAGGAGTAAAGTTCCCTCAGGCTATGCAAAAAGAGAT 660

QY 661 CCGTCTGTATCTTTCGAGGGAGGCTTCCAGCATTCCTTCGGTGTGTGAAGCC 720

DB 661 CCGTCTGTATCTTTCGAGGGAGGCTTCCAGCATTCCTTCGGTGTGTGAAGCC 720

QY 721 ACGAAGGTTGGTCCCATCGAAGTTTGGGTTTTCGGCCACAGCCCGCGAGATGGCT 780

DB 721 ACGAAGGTTGGTCCCATCGAAGTTTGGGTTTTCGGCCACAGCCCGCGAGATGGCT 780

QY 781 CCGTGGCCCGCTCAGGTTTCGGGGTTTCCCGCAGGGGCTCGCTAAGTAGCGGCC 840

DB 781 CCGTGGCCCGCTCAGGTTTCGGGGTTTCCCGCAGGGGCTCGCTAAGTAGCGGCC 840

QY 841 AGGTTTAAACGTTGTGTCAACGGGACCCGAGCCCCCGGATGCCCTGGGGGCGGTGATCA 900

DB 841 AGGTTTAAACGTTGTGTCAACGGGACCCGAGCCCCCGGATGCCCTGGGGGCGGTGATCA 900

QY 901 GTACCAATGTTAATAAGCCCGGCTGTGTGCGCAAAAAAAAAAAAAA 945

DB 901 GTACCAATGTTAATAAGCCCGGCTGTGTGCGCAAAAAAAAAAAAAA 945

RESULT 2  
ANV25877

AAV25877 standard; cDNA; 946 BP.

AAV25877;

17-JUL-1998 (first entry)

cDNA for human Bcl-XL/Bcl-2 associated death promoting polypeptide.

Human; Bcl-XL/Bcl-2 associated death promoting polypeptide; Bad;

programmed cell death; apoptosis; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 52..558

/\*tag= a

/product= "Bad"

NO9812328-A2.

26-MAR-1998.

18-SEP-1997; 97WO-US016991.

20-SEP-1996; 96US-00717123.

(IDUN-) IDUN PHARM INC.

Horne WA, Oltersdorf T;

WPI; 1998-217267/19.

P-PSDB; AAW55779.

Bad gene mediating apoptosis - used to develop products for treating e.g.

neurodegenerative disease, cancers or autoimmune disease.

Claim 2; Fig 1; 4lpp; English.

The present sequence encodes the human Bcl-XL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-XL results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as cancers, e.g. lymphoma and hormone dependent tumours, autoimmune diseases, e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis and viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad can also be used for detection and diagnosis

Sequence 946 BP; 186 A; 295 C; 309 G; 156 T; 0 U; 0 Other;

Query Match 99.7%; Score 942.8; DB 2; Length 946;

Best Local Similarity 99.8%; Pred. No. 4.8e-225; Matches 944; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	61	ATCCAGAGTTTTCAGCCGAGTGAGAGAGAGTCCAGCTTCGACAGAGGGGCTGGGC	120
Qy	121	CCGAGCCCCGAGGGGAGGGGCTTCAGGCTCCGGCAAGCATCATCGCCAGAGGCCAGGC	180
Db	121	CCGAGCCCCGAGGGGAGGGGCTTCAGGCTCCGGCAAGCATCATCGCCAGAGGCCAGGC	180
Qy	181	CTCCTGTGGAGCCCGAGTCCAGAGAGGAGAGCCAAACAGAGCAGCCATCATGGAGGC	240
Db	181	CTCCTGTGGAGCCCGAGTCCAGAGAGGAGAGCCAAACAGAGCAGCCATCATGGAGGC	240
Qy	241	GCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTTACCCCGGGCGGAGAGAGCAC	300
Db	241	GCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTTACCCCGGGCGGAGAGAGCAC	300
Qy	301	GAAGGATGGGGAGGAGAGCCCGCTTCGGGGGCGCTCGGCTCGGGGCGCCCGAAC	360
Db	301	GAAGGATGGGGAGGAGAGCCCGCTTCGGGGGCGCTCGGCTCGGGGCGCCCGAAC	360
Qy	361	CTCTGGCAGCAGACGCTATGGCGCGAGCTCCGAGAGTCCGACAGTGTGTGGAC	420
Db	361	CTCTGGCAGCAGACGCTATGGCGCGAGCTCCGAGAGTCCGACAGTGTGTGGAC	420
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Db	421	TCCTTTAAGAGGGAGTTCCTGCGCCGAGAGAGCGGGGACAGAGCAGATGGGCA	480
Qy	481	AGCTCAGCTGGAGCGGAGTCTTCCAGTCTCTGGTGGATCGGAATTTGGGAGGGAGC	540
Db	481	AGCTCAGCTGGAGCGGAGTCTTCCAGTCTCTGGTGGATCGGAATTTGGGAGGGAGC	540
Qy	541	TCCGCCCCCTCCAGAGTACCTTCGGTCCACATCCCGAATCCACCCGTTCCCATTCGCT	600
Db	541	TCCGCCCCCTCCAGAGTACCTTCGGTCCACATCCCGAATCCACCCGTTCCCATTCGCT	600
Qy	601	GGCAGCCATTTGAATATGGAGGAGTAAAGTTCCCTCAGGCTATGCAAAAAGAGAT	660
Db	601	GGCAGCCATTTGAATATGGAGGAGTAAAGTTCCCTCAGGCTATGCAAAAAGAGAT	660
Qy	661	CGTGTGTATTCCTTTGGAGGGAGGGTTGACCCAGATTCCTTCGGTGTGTGAAGCC	720
Db	661	CGTGTGTATTCCTTTGGAGGGAGGGTTGACCCAGATTCCTTCGGTGTGTGAAGCC	720
Qy	721	ACGGAAGTTGGTCCCATCGGAAGTTTGGGTTTTCGGCCACAGCGCGGAGTGGCT	780
Db	721	ACGGAAGTTGGTCCCATCGGAAGTTTGGGTTTTCGGCCACAGCGCGGAGTGGCT	780
Qy	781	CGTGGCCCCGCTCAGGTTCCGGGGTTTCCCGAGGGGCTCGCTAAGTAGAGAGCC	840
Db	781	CGTGGCCCCGCTCAGGTTCCGGGGTTTCCCGAGGGGCTCGCTAAGTAGAGAGCC	840



Db 781 CCGTGGCCCGCCCTCAGGTTCCGGGGTTTCCGCCAGGCGCCTGGCGCTAAGTAGCGAGCC 840  
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Db 841 AGGTTTAACCGTGTGTCAACGGGACCCGAGCCCGCGATGCCCTGGGGGCGGTGATCA 900  
Qy 901 GTACCAATGTTAATAAGCCCGCGTGTGTGCCCAAAAAAAAAAAAAA 946  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
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Run on: May 28, 2004, 22:04:17 ; Search time 499 Seconds  
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Title: US-09-922-378-1  
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Scoring table: IDENTITY\_NUC  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	945	99.9	945	15	US-10-209-967-1	Sequence 2, Appl1
4	840.4	88.1	1105	9	US-09-894-657-2	Sequence 369, App
5	833	88.1	1127	13	US-10-388-360-369	Sequence 259, App
6	799	84.5	953	10	US-09-873-367C-259	Sequence 646, App
7	799	84.5	971	17	US-10-641-643-646	Sequence 587, App
8	546	57.7	842	16	US-10-264-049-587	Sequence 27567, A
9	400	42.3	477	10	US-09-918-995-27567	Sequence 25409, A
10	381.2	40.3	449	10	US-09-918-995-26409	Sequence 3, Appl1
11	344	36.4	1454	5	US-09-880-107-355	Sequence 355, App
12	267.2	28.2	445	9	US-10-209-967-3	Sequence 3437, App
13	211.4	22.3	303	9	US-09-783-590-3437	Sequence 3465, App
14	201.2	21.3	388	9	US-09-783-590-3465	Sequence 166, App
15	175.6	18.6	235	9	US-09-833-381-166	Sequence 12, Appl
16	106.2	11.2	17580	15	US-10-240-452-12	Sequence 11, Appl
17	98.6	10.4	17580	10	US-10-240-452-11	Sequence 12, Appl
18	64.4	6.8	880	10	US-09-989-993-12	Sequence 13280, A
19	60	6.3	60	10	US-09-908-975-13280	Sequence 165125, A
20	59.8	6.3	848	13	US-10-027-632-165125	Sequence 165125, A
21	59.8	6.3	848	16	US-10-027-632-165125	Sequence 725, App
22	49.2	5.2	108	9	US-09-728-445-725	Sequence 499, App
23	47.6	5.0	80	12	US-10-384-245-499	Sequence 2538, App
24	43.4	4.6	3138	15	US-10-156-761-2538	Sequence 1, Appl1
25	43.4	4.6	9025608	15	US-10-156-761-1	Sequence 5083, App
26	43.2	4.6	4266	15	US-10-156-761-5083	Sequence 28, Appl
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# ALIGNMENTS

RESULT 1  
 US-09-922-378-1  
 ; Sequence 1, Application US/09922378  
 ; Patent No. US20020037869A1  
 ; GENERAL INFORMATION:

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; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-378-1

Query Match      100.0%; Score 946; DB 9; Length 946;
Best Local Similarity 100.0%; Pred. No. 5.5e-267;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGCTTAGGGCGGGGCTCAGGGGCTCAGATCGGGCTTGGGCCCGCAGAGCATGTTCAG 60
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Qy 61 ATCCAGAGTTTCAGCCGAGTGACAGAGAGACTCCAGCTCTGCAGAGAGGGGCTGGGC 120
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RESULT 2

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; Sequence 1, Application US/10066179  
; Publication No. US20020115631A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428C1  
; CURRENT APPLICATION NUMBER: US/10/066.179  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 946  
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US-10-066-179-1

Query Match 100.0%; Score 946; DB 14; Length 946;  
Best Local Similarity 100.0%; Pred. No. 5.5e-267;  
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 481 AGCTCCAGCTGAGCGGAGTTCCTCAGTCTCTGGTGGGATCGGAACCTTGGCAGGGAGC 540  
Db 481 AGCTCCAGCTGAGCGGAGTTCCTCAGTCTCTGGTGGGATCGGAACCTTGGCAGGGAGC 540  
Qy 541 TCGGCCCTCCCGAGTGACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTCGCCT 600  
Db 541 TCGGCCCTCCCGAGTGACCTTCGGTCCACATCCCGAAATCCACCCGTTCCCATTCGCCT 600  
Qy 601 GGGCAGCATTTTGAATATGGGAGGAGTAAGTTCCCTCAGGCTTATGCAAAAGAGAT 660  
Db 601 GGGCAGCATTTTGAATATGGGAGGAGTAAGTTCCCTCAGGCTTATGCAAAAGAGAT 660  
Qy 661 CCGTCTGTATCTTTCGAGGAGGAGTTCAGCCAGATTCCTTCGGGTGTGTGAAGCC 720  
Db 661 CCGTCTGTATCTTTCGAGGAGGAGTTCAGCCAGATTCCTTCGGGTGTGTGAAGCC 720  
Qy 721 ACGGAAGTTGGTCCCATCGGAAGTTTGGGTTTTCGCCCCACAGCCCGGAGAGTGGCT 780  
Db 721 ACGGAAGTTGGTCCCATCGGAAGTTTGGGTTTTCGCCCCACAGCCCGGAGAGTGGCT 780  
Qy 781 CCGTGGCCCCCGCTCAGGTTCCGGGTTTCCCGAGGCGCTTCGCTTAAGTAGCGAGCC 840  
Db 781 CCGTGGCCCCCGCTCAGGTTTCGGGTTTCCCGAGGCGCTTCGCTTAAGTAGCGAGCC 840  
Qy 841 AGGTTTAAACCGTTGTCTACCGGAGCCCGCGCGATGCCCTGGGGCGGTGATCA 900  
Db 841 AGGTTTAAACCGTTGTCTACCGGAGCCCGCGCGATGCCCTGGGGCGGTGATCA 900  
Qy 901 GTACCAATGTTAATAAGCCCGCTGTGTGCCRAAAAAA 946  
Db 901 GTACCAATGTTAATAAGCCCGCTGTGTGCCRAAAAAA 946



OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:36:04 ; Search time 2957 Seconds  
(without alignments)  
9553.474 Million cell updates/sec

Title: US-09-922-378-1  
Perfect score: 946  
Sequence: 1 gggcctggccgcgggtca.....gtgtgcaaaaaaaaaaaaaa 946

Scoring table: IDENTITY NUC  
Capop 10.0 , Capext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estropl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	778.2	82.3	1001	13	BQ276268	BQ276268 AGENCOURT
2	776.6	82.1	920	12	BG748558	BG748558 602706251
3	766.4	81.0	867	12	BI917840	BI917840 603183966
4	764.8	80.8	873	12	BG742674	BG742674 602633280
5	758.8	80.2	949	12	BG752050	BG752050 602732035
6	751	79.4	880	12	BI756192	BI756192 603024211
7	749.8	79.3	1005	12	BM919507	BM919507 AGENCOURT
8	736	77.8	907	13	BQ933058	BQ933058 AGENCOURT
9	722.2	76.3	933	12	BI669797	BI669797 603293376
10	719.4	76.0	1024	12	BM811187	BM811187 AGENCOURT
11	703	74.3	908	14	CA488765	CA488765 AGENCOURT
12	702.4	74.2	767	14	CA426410	CA426410 UI-H-FEI-
13	697.4	73.7	773	12	BI870839	BI870839 603394732
14	696.4	73.6	764	14	CF541292	CF541292 UI-CF-ECL
15	692.8	73.2	887	14	CA488397	CA488397 AGENCOURT
16	692	73.2	1050	12	BM557474	BM557474 AGENCOURT
17	690.4	73.0	839	12	BI757416	BI757416 603029351
18	688.8	72.8	811	14	CF455210	CF455210 AGENCOURT
19	685.6	72.5	781	12	BM973320	BM973320 UI-CF-ECL
20	678.6	71.7	870	14	CD245697	CD245697 AGENCOURT
21	678	71.7	920	13	BQ963001	BQ963001 AGENCOURT
22	674.8	71.3	1170	12	BM464317	BM464317 AGENCOURT
23	674.2	71.3	888	13	BQ216214	BQ216214 AGENCOURT
24	673.8	71.2	891	9	AI338346	AI338346 gq96908.x
25	672.8	71.1	756	12	BI818504	BI818504 603033005
26	669.6	70.8	727	14	CF126337	CF126337 UI-HF-E70
27	667.4	70.5	807	13	EX415776	EX415776 BX415776
28	665.6	70.4	880	13	BQ989089	BQ989089 AGENCOURT
29	661.4	69.9	791	12	BG289203	BG289203 602384205
30	661.4	69.9	791	12	BG818638	BG818638 602778811
31	658.2	69.6	885	13	BQ420314	BQ420314 AGENCOURT
32	656.4	69.4	907	12	BG522766	BG522766 602365324
33	655.2	69.3	804	12	BI836511	BI836511 603082736
34	648.6	68.6	703	13	EX093156	EX093156 BX093156
35	647	68.4	777	12	BG749431	BG749431 602707745
36	647	68.4	912	13	BUI82782	BUI82782 AGENCOURT
37	641.8	67.8	1125	12	BM805363	BM805363 AGENCOURT
38	638.2	67.5	706	12	BG748336	BG748336 602706585
39	635.4	67.2	691	12	BG707618	BG707618 602670686
40	631.2	66.7	727	12	BGI49833	BGI49833 nae01b04..
41	619	65.4	1100	12	BG282723	BG282723 602405802
42	618.2	65.3	1060	12	BM424198	BM424198 AGENCOURT
43	613.2	64.8	923	14	CA495333	CA495333 AGENCOURT
44	605	64.0	772	12	BG748347	BG748347 602705903
45	603	63.7	722	9	AI813350	AI813350 wj33g09.x

Search completed: May 29, 2004, 00:28:12  
Job time : 3965 secs